

A:Cross-references: EMBL:X61569; NID:947313; PIDN:CAA43767.1; PID:947314
 A:Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A:Accession: S18794
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEZ>
 A:Cross-references: EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID:947316
 A:Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A:Accession: S18801
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEZ>
 A:Cross-references: EMBL:X61572; NID:947333; PIDN:CAA43770.1; PID:947334
 A:Experimental source: strain MGAS624 isolate Germany unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A:Accession: S18798
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEO>
 A:Cross-references: EMBL:X61571; NID:947323; PIDN:CAA43769.1; PID:947324
 A:Experimental source: strain MGAS495 isolate Germany unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 C:Genetics:
 A:Gene: speA3
 C:Superfamily: enterotoxin B
 C:Keywords: exotoxin
 F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
 F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
 Query Match 15.8%; Score 195; DB 2; Length 236;
 Best Local Similarity 26.9%; Pred. No. 8e-08;
 Matches 65; Conservative 51; Mismatches 86; Indels 40; Gaps 12;

OY 8 KIVFIIVILISTYFT-----YHOSKSKDISNVKSDLYATITPYDKDC 54
 DB 2 KMFEVLVTLGLTISGEVFAQQDDPSQJHRSSLVKNLONI---YFLYEGDPVTHENV 57
 55 R-VNFSSTHTLNDITQYRGKDY-YISSEMSYEASQKFRKDDHVDVGL-FYIL-----N 106
 DB 58 KSVQDLSHDLIYNVS---GPNYDKLKTTELKNOEMATLFDKNDIDYGVYHLCYLCEN 114
 OY 107 SHNGEYIYGCTTFAONKNVNH-----KLGNLFTISGSQONLNKLTLEDDIYTFQEDIF 161
 DB 115 AENSACIYGGVT--NHEGHNLEIPKRIYKVSIDG--IOSLSFDITNKKMWTAGELDY 169
 OY 162 KIRKYLMDNKKIY-DATSPVSGRIEIGTKDGKHEQIDLDPSENGRSDIFAKYKNRI 220
 DB 170 KVRKYLMDNKKIYDNGSKETETGKIPKKNKESFWDFFPEP-EFTQSKYLMATYKDNET 228
 OY 221 IN 222
 DB 229 LD 230

RESULT 8
 S18786
 exocoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isolate)
 N:Alternate names: scarlet fever toxin
 C:Species: Streptococcus pyogenes phage
 A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain isolate United Kingdom; strain MGAS496 isolate Germany
 C:Date: 29-Jan-1993 #sequence, revision 29-Jan-1993 #text, change 16-Jul-1999
 C:Accession: S18786; S18787; S18788; S18790; S18795; S18799
 R:Nelson, K.; Schleifert, P. M.; Selander, R. K.; Musser, J. M.
 J. Exp. Med. 174, 1271-1274, 1991
 A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
 A:Reference number: S18782; MUID:92044323; PMID:1940804
 A:Accession: S18786
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEZ>

A:Cross-references: EMBL:X61561; NID:947297; PIDN:CAA43759.1; PID:947298
 A:Experimental source: strain MGAS250 isolate California unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
 A:Accession: S18787
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEA>
 A:Cross-references: EMBL:X61562; NID:947299; PIDN:CAA43760.1; PID:947300
 A:Experimental source: strain MGAS251 isolate California unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
 A:Accession: S18788
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEZ>
 A:Cross-references: EMBL:X61563; NID:947301; PIDN:CAA43761.1; PID:947302
 A:Experimental source: strain MGAS256 isolate California unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
 A:Accession: S18790
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEO>
 A:Cross-references: EMBL:X61564; NID:947305; PIDN:CAA43762.1; PID:947306
 A:Experimental source: strain MGAS285 isolate Colorado unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
 A:Accession: S18792
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEO>
 A:Cross-references: EMBL:X61565; NID:947311; PIDN:CAA43763.1; PID:947312
 A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
 A:Accession: S18795
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEH>
 A:Cross-references: EMBL:X61566; NID:947317; PIDN:CAA43764.1; PID:947318
 A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
 A:Accession: S18799
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NNS>
 A:Cross-references: EMBL:X61567; NID:947325; PIDN:CAA43765.1; PID:947326
 A:Experimental source: strain MGAS496 isolate Germany unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
 C:Genetics:
 A:Gene: speA2
 C:Superfamily: enterotoxin B
 C:Keywords: exotoxin
 F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
 F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>
 Query Match 15.4%; Score 190; DB 2; Length 236;
 Best Local Similarity 26.9%; Pred. No. 1.9e-07;
 Matches 65; Conservative 50; Mismatches 87; Indels 40; Gaps 12;

OY 8 KIVFIIVILISTYFT-----YHOSKSKDISNVKSDLYATITPYDKDC 54
 DB 2 KMFEVLVTLGLTISGEVFAQQDDPSQJHRSSLVKNLONI---YFLYEGDPVTHENV 57
 55 R-VNFSSTHTLNDITQYRGKDY-YISSEMSYEASQKFRKDDHVDVGL-FYIL-----N 106
 DB 58 KSVQDLSHDLIYNVS---GPNYDKLKTTELKNOEMATLFDKNDIDYGVYHLCYLCEN 114
 OY 107 SHNGEYIYGCTTFAONKNVNH-----KLGNLFTISGSQONLNKLTLEDDIYTFQEDIF 161
 DB 115 AENSACIYGGVT--NHEGHNLEIPKRIYKVSIDG--IOSLSFDITNKKMWTAGELDY 169
 OY 162 KIRKYLMDNKKIY-DATSPVSGRIEIGTKDGKHEQIDLDPSENGRSDIFAKYKNRI 220
 DB 170 KVRKYLMDNKKIYDNGSKETETGKIPKKNKESFWDFFPEP-EFTQSKYLMATYKDNET 228
 OY 221 IN 222

Db 229 LD 230

RESULT 9

A:28179

enterotoxin E precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999

C:Accession: A28179

R:Couch, J.L.; Solits, M.T.; Bettley, M.J.

J. Bacteriol. 170, 2954-2960, 1988

A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.

A:Reference number: A28179; MUID:88257005; PMID:3384800

A:Accession: A28179

A:Molecule type: DNA

A:Residues: 1-257 <COU>

A:Cross-references: GB:M21319; NID:g153001; PIDN:AAA26617.1; PID:g153002

C:Superfamily: enterotoxin B

Query Match 15.1%; Score 185.5; DB 2; Length 257;

Best Local Similarity 26.3%; Pred. No. 4.7e-07;

Matches 74; Conservative 45; Mismatches 87; Indels 75; Gaps 15;

1 MKKINIKIYVITVILISTYFTYHQSRRKDIS-----NKSDDL-LYAV-- 44

1 MKRTAFILFLFI--ALTLTSPLVNKGSEKEINERKKSSELQNALSLNRQIYYNE 58

45 -TTPYKRCRV-----NFSTH---TLNID-----TQYKGRDYISSEMSYE 85

59 KATENKESDDOFLNTLFKGFETGHPWYNDLVLDGSKDATTNKKYKGG----- 107

86 ASQKFRKRDHVDVFGFLYILNSHTG-----EYIYGITPAQNNKYNH--KILGNLFISGE 138

108 -----KVDLGAVYGCACAGTTPNKTACMTGGVTLHDNNKLTTEKKVPINLWIDGK 158

139 SOONLNKILKEDIYFOEDIRKRYLMDNRYKIVATSPYSGRIEIG-----TDDGK 193

159 QTVPIIDKXVTSKKEVYQELDQARHYLHGKRGFLYNSDS--FEGKQKRGILVHSESGS 216

194 HEQIDLFSPNEGRSDIFAK-YKDNRIINMKNSHFDIYL 233

217 TVSYDLFDA--QGGYPTQLRIYRDNKNTINSENL-HIDLYL 254

Db

Db

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OY 109 -----TG--EYIGGTPAQNKNVHKLGNLFISGESQONLNKLTLE----KD 152

122 FSSKDNNGKVTGGCTCMTGGITTKHEGHNFDGNLQNLV--RYENKRNITSEFVOTDK 179

153 IVTFQEDIFKIRKYLMDNRYKID-ATSPYSGRIEIGTKDQKHEQIDLFSPNKG-TRSD 210

180 SVTQELDIFARNLNKLNRYENFSPYEGYIKFLENNGNFWMYMPAPGDKFQSK 239

211 IFAKYKDNRIINMKN 225

240 YLMYNDNKTVDKSKS 254

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